BRE1206: Towards Generating Multiple-Fungal Disease Resistance in Lentil

Lentil production has been affected by three major foliar diseases over the past two decades, Ascochyta blight caused by *Ascochyta lentis*, Anthracnose caused by *Colletotrichum lentis,* and Stemphylium blight caused by *Stemphylium botryosum*. No resistance to the more aggressive and widespread race 0 of the A nthracnose pathogen has been identified in cultivated lentils, erosion of resistance to the Ascochyta blight fungus has been observed, and resistance to Stemphylium blight in cultivated lentils is low and complex. A wild relative of lentil, *Lens ervoides*, has emerged as a valuable source of resistance to these pathogens, and crossing of it with lentil varieties has been made possible through special techniques such as embryo rescue. However, the tracing of, and selection for these genes from the wild relative among the hundreds and thousands of offspring from such crosses during the early generations of the breeding process remain a problem. Conventional pathogenicity testing is not feasible then because of high numbers of individuals and lines in early generations, so tags associated with such genes (molecular markers) have proven useful in such situations in other systems. The development of such tags is not possible in populations developed from crosses of the wild and cultivated species, but is feasible in those from a cross of two wild parents, as was done in this project. This population was genetically characterized which allowed us to develop a genetic map that we used as a guide to locations in the genome that are associated with disease resistance. For this purpose, the population was also screened for resistance to all three diseases, which allowed us to identify eight locations on the genetic map that are associated with Anthracnose resistance and three locations associated with Stemphylium blight resistance. These locations are hot spots for resistance gene candidates, so with the help of genome information generated earlier in Dr. Bett's group, we could catalogue all the genes located at these hot spots. It was not possible to use the genetic map to locate hot spots for resistance gene candidates for Ascochyta blight, so we used two other approaches to identify genes or their products involved in resistance. In the first approach, we monitored the expression of genes specifically activated or suppressed in resistant compared to susceptible lines after their infection with the respective pathogen. In the second approach, rather than looking at gene expression, we monitored what proteins (the product of expressed genes) were synthesized and in what quantities in the wild lentil lines after challenge with those pathogens. In addition to molecular markers associated with the hot spots on the genetic map, these latter two approaches, together with the information provided by the genetic map, allowed us to identify 24 gene candidates for Ascochyta blight resistance, 55 gene candidates for Anthracnose resistance, and 45 for Stemphylium blight resistance. We have prioritized 10 candidate genes for resistance to Ascochyta blight, 27 for Anthracnose, and 20 for Stemphylium blight resistance for further validation and testing as molecular markers in the breeding program.